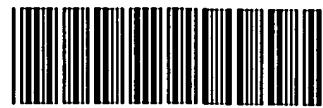


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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/785,607B
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IFW/b

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TIME: 09:04:12

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4 <110> APPLICANT: Ashkenazi, Avi J.
 5 Fong, Sherman
 6 Goddard, Audrey
 7 Gurney, Austin L.
 8 Napier, Mary A.
 9 Tumas, Daniel
 10 Wood, William I.
 12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
 13 THE TREATMENT OF DISEASES CHARACTERIZED BY A-33 RELATED
 14 ANTIGENS
 16 <130> FILE REFERENCE: 39780-1216R1C1D5
 18 <140> CURRENT APPLICATION NUMBER: US 10/785,607B
 19 <141> CURRENT FILING DATE: 2004-02-24
 21 <150> PRIOR APPLICATION NUMBER: US 09/953,499
 22 <151> PRIOR FILING DATE: 2001-09-14
 24 <150> PRIOR APPLICATION NUMBER: US 09/254,465
 25 <151> PRIOR FILING DATE: 1999-03-05
 27 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
 28 <151> PRIOR FILING DATE: 1998-11-20
 30 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
 31 <151> PRIOR FILING DATE: 1998-09-17
 33 <160> NUMBER OF SEQ ID NOS: 30
 35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 37 <210> SEQ ID NO: 1
 38 <211> LENGTH: 299
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
 42 <400> SEQUENCE: 1
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 45 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 46 20 25 30
 47 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 48 35 40 45
 49 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 50 55 60
 51 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 52 65 70 75 80
 53 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 54 85 90 95
 55 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 56 100 105 110
 57 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val

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58	115	120	125	
59	Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr			
60	130	135	140	
61	Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro			
62	145	150	155	160
63	Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn			
64	165	170	175	
65	Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro			
66	180	185	190	
67	Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly			
68	195	200	205	
69	Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser			
70	210	215	220	
71	Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val			
72	225	230	235	240
73	Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly			
74	245	250	255	
75	Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly			
76	260	265	270	
77	Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu			
78	275	280	285	
79	Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val			
80	290	295		
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84	<211> LENGTH: 321			
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86	<213> ORGANISM: Homo sapiens			
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90	1	5	10	15
91	Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro			
92	20	25	30	
93	Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly			
94	35	40	45	
95	Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro			
96	50	55	60	
97	Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala			
98	65	70	75	80
99	Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val			
100	85	90	95	
101	Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr			
102	100	105	110	
103	Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp			
104	115	120	125	
105	Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr			
106	130	135	140	
107	Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg			
108	145	150	155	160
109	Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile			

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112	180	185	190
113	Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser		
114	195	200	205
115	Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp		
116	210	215	220
117	Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys		
118	225	230	235
119	240	245	250
120	Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr		
121	255	260	265
122	Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly		
123	270	275	280
124	Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile		
125	285	290	295
126	Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile		
127	300	305	310
128	Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala		
129	315	320	325

129 Arg

133 <210> SEQ ID NO: 3

134 <211> LENGTH: 390

135 <212> TYPE: DNA

136 <213> ORGANISM: Artificial Sequence

138 <220> FEATURE:

139 <223> OTHER INFORMATION: Consensus DNA Sequence

141 <400> SEQUENCE: 3

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143	ttgtatggtc	tctgaggaag	gcggcaacag	ctatggggag	gtcaaggtca	agctcatcgt	120
144	gcttgcct	ccatccaagc	ctacagttaa	catccccccc	tctgccccca	ttgggaacccg	180
145	ggcagtgcgt	acatgctcag	aacaagatgg	ttccccaccc	tctgaataca	cctggttcaa	240
146	agatggata	gtgatgccta	cgaatcccaa	aagcaccctgt	gccttcagca	actcttccta	300
147	tgtccctgaat	cccacaacag	gagagctgg	ctttgatccc	ctgtcagcct	ctgataactgg	360
148	agaatacagc	tgtgaggcac	ggaatggta				390

150 <210> SEQ ID NO: 4

151 <211> LENGTH: 726

152 <212> TYPE: DNA

153 <213> ORGANISM: Artificial Sequence

155 <220> FEATURE:

156 <223> OTHER INFORMATION: Consensus DNA Sequence

158 <400> SEQUENCE: 4

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160	ctgttgtgtct	cagggtgcggc	tgatcgcat	ggggacaaag	gcgcacgctc	gagaggaaac	120
161	tgttgtgcct	ttccatattt	gcgcattctgt	tgtgctccct	ggcattgggc	agtgttacag	180
162	ttgcactctt	ctgaacctga	agtcagaatt	cctgagaata	atccgtgtaa	gttgtccctgt	240
163	gcctactcgg	gttttcttc	tccccgtgt	gagtggaaat	ttgaccaagg	agacaccacc	300
164	agactcggtt	gtataataaa	caagatcaca	gcttcctatg	aggaccgggt	gaccttcttg	360
165	ccaactggta	tcaccttcaa	gtccgtgaca	cgggaaagaca	ctgggacata	cacttgtatg	420
166	gtctctgagg	aaggcggcaa	cagctatggg	gaggtcaagg	tcaagctcat	cgtgcttgc	480

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167 cctccatcca agcctacagt taacatcccc tcctctgcc a ccattggaa ccgggcagt 540
168 ctgacatgct cagaacaaga tggttccca ccttctaat acacctggg caaagatggg 600
169 atagtgatgc ctacgaatcc caaaaggacc cgtgcctca gcaactctc ctatgtcctg 660
170 aatcccacaa caggagagct ggtcttgat cccctgtcag cctctgatac tggagaatac 720
171 agctgt 726
173 <210> SEQ ID NO: 5
174 <211> LENGTH: 1503
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Consensus DNA Sequence
181 <400> SEQUENCE: 5
182 gcaggcaaag taccaggccc gcctgcattt gaggccacaag gttccaggag atgtatccct 60
183 ccaattgagc accctggaga tggatgaccg gagccactac acgtgtgaag tcacctggca 120
184 gactcctgat ggcaacccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
185 ctctgtctcc aagcccacag tgacaactgg cagcggttat ggcttcacgg tgccccaggg 240
186 aataggatt agcctcaat gccagggttc ggggttctcc tcccatcagt tatatttgg 300
187 ataagaaca gactaataac cagggAACCC atcaaaggtag caaccctaag tactttactc 360
188 ttcaaggctg cggtgatagc cgactcaggc tcctatttct gcactgccaa gggccagg 420
189 ggctctgagc agcacagcga cattgtgaag tttgtggta aagactcctc aaagctactc 480
190 aagaccaaga ctgaggcacc tacaaccatg acataccct taaaagcaac atctacagt 540
191 aagcagtcc gggactggac cactgacatg gatggctacc ttggagagac cagtgtggg 600
192 ccagggaaaga gcctgcctgt ctttgcattc atcctcatca tctccttgc ctgtatggg 660
193 gttttacca tggcctatcatcatgatctgtt cggaaagacat cccaaacaaga gcatgtctac 720
194 gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaccat ggggtggcc 780
195 atcttcgcaa gtggctgctc cagtgatgag ccaacttccc agaatctgg gcaacaacta 840
196 ctctgatgag ccctgcatac gacaggagta ccagatcatc gcccagatca atggcaacta 900
197 cggccgcctg ctggacacag ttcctctggat ttaggatctt ctggccactg agggcaaaag 960
198 tgtctgttaa aatgccccca tttaggccagg atctgctgac ataattgcct agtcagtcct 1020
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202 ctggacttcc tctctaaata ccagaggaa gatgcccata gcactaggac ttggtcatca 1260
203 tgcctacaga cactattcaa ctttggcatc ttgccaccag aagaccgcg gggaggctca 1320
204 gctctgccag ctcagaggac cagctatatac caggttatttctt cagggccaga 1380
205 cagctttaa ttgaaatttgc tatttcacag gccagggttc agttctgctc ctccactata 1440
206 agtctaattgt tctgactctc tcctggtgct caataaatat ctaatcataa cagcaaaaaaa 1500
207 aaa 1503
209 <210> SEQ ID NO: 6
210 <211> LENGTH: 319
211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 6
215 Met Val Gly Lys Met Trp Pro Val Leu Trp Thr Leu Cys Ala Val Arg
216 1 5 10 15
217 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
218 20 25 30
219 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
220 35 40 45

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221 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
 222 50 55 60
 223 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
 224 65 70 75 80
 225 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
 226 85 90 95
 227 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
 228 100 105 110
 229 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
 230 115 120 125
 231 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
 232 130 135 140
 233 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
 234 145 150 155 160
 235 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
 236 165 170 175
 237 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
 238 180 185 190
 239 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
 240 195 200 205
 241 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
 242 210 215 220
 243 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
 244 225 230 235 240
 245 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
 246 245 250 255
 247 Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
 248 260 265 270
 249 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
 250 275 280 285
 251 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
 252 290 295 300
 253 Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His Leu Asp Gln
 254 305 310 315
 257 <210> SEQ ID NO: 7
 258 <211> LENGTH: 2181
 259 <212> TYPE: DNA
 260 <213> ORGANISM: Homo sapiens
 262 <400> SEQUENCE: 7
 263 cccacgcgtc cgcccacgca tccgcccacg ggtccgcccc caaccagaag 60
 264 tttgagcctc tttggtagca ggaggctgga agaaaggaca gaagtagctc tggctgtat 120
 265 ggggatctta ctgggcctgc tactcctggg gcacctaaca gtggacactt atggccgtcc 180
 266 catcctggaa gtgccagaga gtgtAACAGG accttggaaa gggatgtga atcttcctg 240
 267 cacctatgac cccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
 268 ctcagaccct gtcaccatct ttctacgtga ctcttctggta gaccatatcc agcaggcaaa 360
 269 gtaccaggcgc cgcctgcatg tgagccacaa ggttccagga gatgtatccc tccaaattgag 420
 270 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480
 271 tggcaaccaa gtcgtgagag ataagattac tgagctcgt gtcagaaac tctctgtctc 540
 272 caagcccaca gtgacaactg gcagcggtta tggcttcacg gtgccccagg gaatgaggat 600

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/785,607B

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